

Interleukin (IL)-10 Gene Polymorphisms Are Associated with Type 2 Diabetes With and Without Nephropathy: A Study of Patients from the Southeast Region of Iran

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Abstract—The impact of several environmental and genetic factors on diabetes and its complications is well documented. It has also been established that cytokines play a key role in the regulation of immune responses which have been shown to be important in the pathogenesis of diabetes. Studies showed that single-nucleotide polymorphisms within the –592 region of interleukin-10 (IL-10) are associated with the regulation of expression. In this study, we aimed to find polymorphisms of this region that may be associated to type 2 diabetic (T2D) patients with and without nephropathy. In this study, peripheral blood samples were collected from 100 T2D patients without nephropathy, 100 T2D patients with nephropathy, and 100 healthy controls. DNA was extracted, and a polymerase chain reaction-restriction fragment length polymorphism technique was performed to examine the polymorphisms within the –592 region of IL-10 gene. Our results showed a significant difference between the genotypes and alleles of the –592 region of IL-10 in nephropathic and non-nephropathic patients in comparison to the healthy controls. The differences between the two patient groups in relation to genotypes and alleles were not significant. Results of this study suggest that the functional gene polymorphism of IL-10 reported here may play an important role in the pathogenesis of diabetes, but it seems that these polymorphisms do not have an effect on the nephropathic complications of the disease.

KEY WORDS: IL-10; diabetes; nephropathy; polymorphism.

INTRODUCTION

The frequency of diabetes mellitus is increasing globally, and it is expected that this latent disorder will affect 200 million of people by 2010 and 300 million in 2025 [1]. Type 2, sometimes referred to as non-insulin dependent diabetes mellitus or adult-onset diabetes, is the most prevalent type of the diabetes [2]. Current studies showed that several genetic and environmental parameters are associated with type 2 diabetes (T2D) and its complications [3]. It has been suggested that diabetes is an immune-dependent disease in which the pattern of cytokine expression is changed [4]. As an example, in T2D peripheral blood monocytes produce inappropriate levels of inflammatory cytokines which

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42 may induce the associated pathology of the disease [5].
 43 Subsequently, the cytokine/cytokine–receptor axis has
 44 been the subject of several studies to investigate their
 45 crucial roles in diabetes and its complications [3], and as
 46 a result, the important role of cytokine imbalance in T2D
 47 with and without nephropathy has been reported [6, 7].
 48 Increased serum levels of inflammatory cytokines
 49 including interleukin (IL)-18 [8], IL-6 [9], IFN- γ [7],
 50 IL-17 [7], and TNF- α [9] have been documented in T2D
 51 and its nephropathic complications. Furthermore, the
 52 association of IL-10 in immunological disorders such as
 53 multiple sclerosis [10], systemic lupus erythematosus
 54 [11], nephrotic syndrome [12], graft rejection [13],
 55 asthma [14], and type 1 [15] diabetes is well established.
 56 The key roles of IL-10 as an inhibitory cytokine of
 57 autoimmunity and inflammation [16] raise questions
 58 concerning the impacts of this cytokine on the patho-
 59 genesis of other diseases including T2D and its neph-
 60 ropathic complications. Previous studies showed that the
 61 secretion of IL-10 can be affected by polymorphisms in
 62 its promoter region [17]. Therefore, this study was aimed
 63 to investigate the relation between the polymorphisms of
 64 the -592 region of IL-10 in T2D patients with and
 65 without nephropathy.

66 **MATERIAL AND METHODS**

67 **Subject**

68 Blood samples were collected from 100 type 2
 69 diabetic patients without nephropathy, 100 T2D patients
 70 showing nephropathic complications, and 100 healthy
 71 controls. All the T2D patients were selected from the
 72 Rafsanjan population that had been referred to the
 73 Diabetes Clinic of the Ali Ebn-Abitaleb Hospital. The
 74 T2D patients were selected based on peripheral blood
 75 glucose levels of more than 130 mg/dl, and nephropathy
 76 was assessed in diabetic patients based on proteinuria of
 77 at least 500 mg/24 h and glomerular filtration rates
 78 (GFR) of less than 25 ml/min [18]. GFR were calculated
 79 according to creatinine-based equations [19]. The patient
 80 and control groups were selected from within the
 81 Rafsanjan population with similar medical and demo-
 82 graphic characteristics including duration of diabetes,
 83 sex, age, and socioeconomic status (Table 1). Assess-
 84 ments of socioeconomic conditions were measured
 85 based on the level of education and the monthly income
 86 of donors. Classifications for education were: a donor
 87 holding a diploma was considered weak, an under-

graduate was considered moderate, and a postgraduate 88
 was considered high. Monthly income was classified as: 89
 under \$250, weak; \$250–1,000, moderate; and more 90
 than \$1,000, high. Information regarding lipid levels, 91
 proteinuria, estimate of GFR, and drug therapy of 92
 patients is also listed in Table 1. Human ethical approval 93
 for this study was granted by the Ethical Committee of 94
 the Rafsanjan University of Medical Sciences. Consent 95
 forms were filled out by both patients and controls prior 96
 to blood collection. Previous studies showed that some 97
 factors such as infections [20–22], allergic conditions 98
 [23], and smoking [24, 25] were considered as bias 99
 factors in diabetes and nephropathy; hence, patients with 100
 these bias factors were eliminated from the study using a 101
 questionnaire. 102

Assays 103

Fasting blood sugar, urine albumin level, blood 104
 pressure, and clinical presentations were assessed three 105
 times during a period of 6 months for each patient and 106
 control group. 107

DNA Extraction 108

Peripheral blood was collected on EDTA, and 109
 genomic DNA was extracted using a commercial kit 110
 (Bioneer, Korea) following the manufacturer’s recom- 111
 mended procedures. Extracted DNA was aliquoted (for 112
 each patient sample) and stored at -20°C for further use. 113

Detection of Polymorphisms 114

The IL-10 gene polymorphism (within the gene 115
 promoter) was analyzed by PCR-RFLP method. PCR of 116
 the promoter region of the IL-10 gene was performed in 117
 a volume of 50 μ L containing 5 μ l of *Taq* DNA 118
 polymerase buffer (10 \times), 1.5 μ l of MgCl₂ (stock 119
 concentration, 1.5 mM), 1 μ l of each dNTP [(dATP, 120
 dCTP, dGTP, dTTP) at a stock concentration of 10 mM, 121
 2 μ l of each primer (stock concentration of 25 ng/ μ l), 122
 1 μ l of prepared DNA, and sterile double distilled water 123
 to a final volume of 50 μ l. The sequence of the forward 124
 primer was 5'-GTAATATCTCTGTGCCTC-3', and the 125
 sequence of reverse primer was 5'-CATTCCAGAATA 126
 CAATGG-3'. The amplification was performed using the 127
 following program: 1 cycle of 95°C for 5 min (denatu- 128
 ration), 50 s at 53°C for annealing, 72°C for 40 s 129
 (elongation) followed by 30 cycles of 95°C for 50 s, 50 s 130
 at 53°C for annealing, and 72°C for 40 s using a thermal 131
 cyclers (C1000, Bio-Rad, USA). During the last 45 s of 132

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Table 1. Demographic, Socioeconomic Conditions, and Clinical Parameters of T2D Patients with and without Nephropathy and Controls

Variant	Healthy control	Type 2 diabetic patients without nephropathy	Nephropathic type 2 diabetic patients
Age (years)	40±7	40±9	40±6
Sex			
Female	60 (60%)	59 (59%)	62 (62%)
Male	40 (40%)	41 (41%)	38 (38%)
Duration of diabetes (years)		9±3	10±4
Socioeconomic status			
Weak	22 (22%)	21 (21%)	24 (24%)
Medium	47 (47%)	49 (49%)	46 (46%)
High	31 (31%)	30 (30%)	30 (30%)
Weight (kg)	60±7	50±7	50±9
Drug therapy	–	Metformin	Insulin
Lipid levels			
Triglyceride (mg/dl)	100±4	210±6	350±12
Cholesterol (mg/dl)	150±6	170±5.7	290±10
HDL (mg/dl)	40±3	35±3	24±2
LDL (mg/dl)	100±9	140±6	180±11
Glucose level (mg/dl)	95±105	140–190	160–205
Proteinuria (mg/dl)	25±1.5	36.6±3	899±50 ^a
Estimated GFR	120±5	101±5	72±3 ^b

^a Significant difference in proteinuria ($p < 0.002$, t test, case vs. control). Data are shown as mean±SE
^b Significant difference in estimated GFR ($p < 0.001$, t test, case vs. control). Data are shown as mean±SE

133 the first stage, 0.3 µl of *Taq* DNA polymerase (5 units)
 134 was added to the mixture. The amplified PCR product of
 135 promoter region of the IL-10 gene covers the –592
 136 region and has a molecular size of 437 bp. The *Rsa*-1
 137 (Fermentase, Finland) restriction site, which was used to
 138 detect polymorphisms, is internal to the –592 region
 139 which was examined here. *Rsa*-1-sensitive fragments
 140 were digested into 236 and 201 bp sub-fragments. In the
 141 case of heterozygotic patients with the *A/C* alleles, the
 142 digest gave rise to three different fragments of 201 and
 143 236 bp and the undigested, 437 bp. In the homozygotic
 144 form, a single 437-bp fragment (*C/C* alleles) or the two
 145 201- and 236-bp bands (*A/A* alleles) were observed. The
 146 digested products were run on a 2.5% agarose gel
 147 (CinnaGen, Iran) and analyzed using a ChemiDoc XRS
 148 System (Bio-Rad, USA) after staining with ethidium
 149 bromide.

150 **Statistical Analysis**

151 Hardy–Weinberg equilibrium was assessed using
 152 the genotype data. Allele and genotype frequencies were
 153 calculated in patients and healthy controls by direct gene
 154 counting. Statistical analysis of the differences between
 155 groups was determined by the χ^2 test using EPI 2000
 156 and SPSS software version 13. A p value of less than
 157 0.05 was considered significant.

RESULTS

158 Evaluation of polymorphisms within the –592
 159 region of the IL-10 gene by *Rsa*-1 restriction digestion
 160 showed that the prevalence of the *C/C*, *A/C*, and *A/A*
 161 genotypes was 60 (60%), 36 (36%), and 4 (4%) in non-
 162 nephropathic T2D patients, respectively (Table 2). Our
 163 results also revealed that the frequency of *C/C*, *A/C*, and
 164 *A/A* genotypes was 47 (47%), 47 (47%), and 6 (6%) in
 165 nephropathic T2D patients, respectively (Table 3). These
 166 values for the control group were 22 (22%), 55 (55%),
 167 and 23 (23%), respectively (Tables 2 and 3). Statistical
 168 analysis showed that the difference between diabetic
 169 (nephropathic and non-nephropathic) groups in compar-
 170 ison to the control group in relation to these genotypes
 171 was significant ($p = 0.001$). Our results also showed that
 172 the frequency of *C* allele was 156 (78%), and the *A*
 173 allele was 44 (22%) in non-nephropathic T2D patients.
 174 The frequency of *C* and *A* alleles was 141 (70.5%) and
 175 59 (29.5%), respectively, in T2D patients with nephrop-
 176 athy (Table 2). Evaluation of the control group showed
 177 that the frequency of the *C* allele was 99 (49.5%), and
 178 the *A* allele was 101 (50.5%) in this group (Tables 2 and
 179 3). Statistical analysis regarding these alleles showed
 180 that the difference between patients (nephropathic and
 181 non-nephropathic) in comparison to the control group
 182 was also significant ($p = 0.001$; Tables 2 and 3).
 183

Table 2. Frequency of Genotypes within the -592 Region of the IL-10 Gene in Non-nephropathic T2D Patients and Controls

Condition	Patients	Control	<i>p</i> value
Genotype, <i>n</i> (%)			
<i>C/C</i>	60 (60%)	22 (22%)	<i>p</i> =0.001
<i>A/C</i>	36 (36%)	55 (55%)	
<i>A/A</i>	4 (4%)	23 (23%)	
Alleles, <i>n</i> (%)			
<i>C</i>	156 (78%)	99 (49.5%)	<i>p</i> =0.001
<i>A</i>	44 (22%)	101 (50.5%)	

Statistical analysis showed that the frequency of the genotypes and alleles in T2D patients without nephropathy was not different from the T2D patients with nephropathy (*p*=0.27; Table 4). Our results showed that the difference between the groups in relation to age, sex, and socioeconomic conditions was not significant (Table 1).

DISCUSSION

The crucial role of cytokine networks in orientating immune responses is well documented [26]. Several factors such as infectious agents, hormonal conditions, and cytokine gene polymorphisms regulate expression and secretion of cytokines [27]. The main etiological cause of T2D and its inflammatory complications, such as nephropathy, has yet to be clarified. Some investigators suggested that immune-related factors play important roles in etiology and pathogenesis of T2D and its associated renal complications [28]. As clearly indicated in Table 1, both patients and control groups were demographically matched. Our findings indicated a significant difference between T2D patients with and without nephropathy when compared

Table 3. Frequency of Genotypes within the -592 Region of the IL-10 Gene in Nephropathic T2D Patients and Controls

Condition	Patients	Control	<i>p</i> value
Genotype, <i>n</i> (%)			
<i>C/C</i>	47 (47%)	22 (22%)	<i>p</i> =0.001
<i>A/C</i>	47 (47%)	55 (55%)	
<i>A/A</i>	6 (6%)	23 (23%)	
Alleles, <i>n</i> (%)			
<i>C</i>	141 (70.5%)	99 (49.5%)	<i>p</i> =0.001
<i>A</i>	59 (29.5%)	101 (50.5%)	

Table 4. Comparison of the Frequency of Genotypes and Alleles within the -592 Region of the IL-10 Gene Between Nephropathic and Non-nephropathic T2D Patients

Condition	Nephropathic T2D patients	Non-nephropathic T2D patients	<i>p</i> value
Genotype, <i>n</i> (%)			
<i>C/C</i>	47 (47%)	60 (60%)	<i>p</i> =0.27
<i>A/C</i>	47 (47%)	36 (36%)	
<i>A/A</i>	6 (6%)	4 (4%)	
Alleles, <i>n</i> (%)			
<i>C</i>	141 (70.5%)	156 (78%)	<i>p</i> =0.27
<i>A</i>	59 (29.5%)	44 (22%)	

to healthy controls regarding both genotypes and alleles of the -592 region of the IL-10 gene. Our data revealed that there are no significant differences between the two T2D patient groups; therefore, based on the current results, it can be concluded that the polymorphisms described here are associated with T2D rather than its nephropathic complications in our studied population (southeast Iranian patients). In other words, T2D patients from the Rafsanjanese region show a significant correlation between their disease and the IL-10 -590 polymorphism.

In contradiction to our data presented here, Ezzidi *et al.* showed that the polymorphisms in -592 region of the IL-10 gene are not associated with nephropathic complication in T2D [29]. These finding supported earlier conclusions reported by Scarpelli *et al.*, who had also shown that these polymorphisms are not associated with T2D [30]. On the other hand, Chang *et al.* reported a significant relationship between T2D without nephropathy and healthy controls regarding the -592 region of the IL-10 gene [31]. In addition, Mtraoui *et al.* reported that the IL-10 promoter polymorphisms of the -1082, -819, and -592 regions are associated with nephropathy complications in T2D [32]. Kolla *et al.* also demonstrated that the polymorphisms within the -1082 region of the IL-10 gene are associated with peripheral neuropathy in South Indian T2D patients [33].

The discrepancies between our results and those of other research groups may be due to differences in the populations that were studied; some of the groups are comprised of different races and genetic backgrounds. It seems that *C/C* genotype is associated with T2D in Rafsanjanese population, and probably, the *C/C* genotype can be considered as a risk factor for the population.

Q3

Q4

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241 Interestingly, our previous study on another anti-
 242 inflammatory cytokine (IL-4) showed that T2D patients
 243 with nephropathic complication, but not T2D without
 244 nephropathy, are significantly associated with IL-4
 245 polymorphisms [34]. Therefore, based on the results of
 246 our current and previous studies, it may be concluded
 247 that the polymorphisms in IL-10 can affect the onset of
 248 T2D, but not nephropathic complication in Rafsanjane
 249 patients, while IL-4 polymorphisms may be correlated to
 250 nephropathy in the T2D patients.

251 In conclusion, nephropathic complications of T2D
 252 are very complex; apart from the myriad of cytokines
 253 discussed here and reported elsewhere, there is also an
 254 association with several environmental and other genetic
 255 factors. Significant studies are required to investigate all
 256 these parameters and how they influence each other
 257 before we can have a comprehensive understanding of
 258 the disorder.

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UNCORRECTED PROOF